

Sub 1
cont

c) ~~subjecting said libraries to affinity or functional selection steps to generate artificial SH3 domains.~~

2. (amended) The method according to claim 1, wherein step a) comprises replacing amino acid residues in a variable region of the RT-loop with a random combination of any other amino acid residues.

3. (amended) The method according to claim 2, wherein the amino acid residues in the variable region of the RT-loop that are replaced comprise six amino acid residues that immediately follow a conserved stretch of amino acids having an ALYDY (SEQ ID NO:1) consensus sequence.


4. (amended) The method according to claim 1, wherein the recombinant libraries comprise said RRT-SH3 domains in plasmid, phagemid or viral vectors.

2 Please add the following new claims 17-19

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cont

--17. The method according to claim 3, wherein the six amino acids that are replaced in the RT-loop are replaced with a peptide motif selected from the group consisting of XSWSXX (SEQ ID NO:28), XSPFXX (SEQ ID NO:30) and XSXFPW (SEQ ID NO:32), wherein X is any amino acid.

18. The method of claim 17, wherein X is an amino acid selected from the group consisting of V, F, D, M, P, S, T, W, and Y (SEQ ID NOS:29 and 30).

 19. The method of claim 17, wherein the peptide motif is selected from the group consisting of VSWSPD (SEQ ID NO:6), FSWSDT (SEQ ID NO:7), DSWSTS (SEQ ID NO:8), YSWSDM (SEQ ID NO:9), WSPFPS (SEQ ID NO:10), DSPFSF (SEQ ID NO:11), FSPFSF (SEQ ID NO:12), FSPFDW (SEQ ID NO:13), SSPFDW (SEQ ID NO:14), YSPFSW (SEQ ID NO:15), TSPFPW (SEQ ID NO:16), YSFFPW (SEQ ID NO:17), YSDFPW (SEQ ID NO:18) and DSWFPW (SEQ ID NO:19).--
